SEQUENCE LISTING

<110> Andrade-Gordon, Patricia
Darrow, Andrew L.
Qi, Jenson

<120> DNA encoding human serine protease C-E

<130> ORT-1030

<140>

<141>

<160> 11

<170> PatentIn Ver. 2.0

<210> 1

<211> 1430

<212> DNA

<213> Homo sapiens

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<210> 2

<211> 1166

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C-E catalytic domain in a zymogen activated construct

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gtggacgcgg ccgctcttgc tgccccctt gatgatgatg acaagatcgt tgggggctat 180

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aacctgaaca aaccatacct gttctctgtg ctgctggggg cctggcagct ggggaaccct 360

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aaggaaggtg cctgtgcaga cattgccctg gtgcgtctcg agcgctccat acagttctca 480

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<210> 3

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer
oligonucleotide

<400> 3

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<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer
oligonucleotide

<400> 4

tccgggcccc cagaggtaga tgag 24

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer
oligonucleotide

<400> 5

ctgcagaagc tgaaggttcc 20

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer
oligonucleotide

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cagagaggct gatgtagacc 20

<210> 7

<211> 317

<212> PRT

<213> Homo sapiens

<400> 7

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly
1 5 10 15

Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala
20 25 30

Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn
35 40 45

Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile
50 55 60

Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu
65 70 75 80

Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu
85 90 95

Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly
100 105 110

Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu Pro
115 120 125

His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala Leu
130 135 140

Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro Ile
145 150 155 160

Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys Trp
165 170 175

Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro
180 185 190

Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys

195 200 205

Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp

210 215 220

Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly

225 230 235 240

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu Leu

245 250 255

Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg Pro

260 265 270

Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile

275 280 285

Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala Leu

290 295 300

Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala Arg Ser

305 310 315

<210> 8

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C-E catalytic domain fusion protien

<400> 8

Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu Leu

1 5 10 15

Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys

20 25 30

Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp

35 40 45

Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Asp Ser Glu Trp Pro

50 55 60

Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser

65 70 75 80

Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp

85 90 95

Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln

100 105 110

Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val

115 120 125

Glu Pro His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile

130 135 140

Ala Leu Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu

145 150 155 160

Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His

165 170 175

Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro

180 185 190

His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu

195 200 205

Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr

210 215 220

Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys

225 230 235 240

Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp

245 250 255

Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn

260 265 270

Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu

275 280 285

Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly

290 295 300

Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala Arg Ser Ser

305 310 315 320

Arg His His His His His His

325

<210> 9

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nested primer oligonucleotide

<400> 9

ggacatgctg tgtgccggct acttggaggg ggagcgggat 40

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer oligonucleotide

<400> 10

aggatctaga ggacagcgag tggccctgga tcg 33

<210> 11

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer oligonucleotide

<400> 11

gtgctctaga ggagcgcgcg gcggccccag agc 33